

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- ✓ BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

COPY

SEQUENCE LISTING

<110> Thomashow, Linda S.

Delaney, Shannon M.

Mavrodi, Dmitri V.

Weller, David M.

<120> Sequences Encoding PhzO and Methods

<130> 0229.99

<150> US 60/236,634

<151> 2000-09-29

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 2869

<212> DNA

<213> Pseudomonas chlororaphis

<220>

<221> CDS

<222> (89)..(1564)

<223>

<220>

<221> gene

<222> (76)..(1564)

<223>

<220>

<221> RBS

<222> (76)..(81)

<223>

<400> 1
tcgactctag aacgttgtcc ttgacccagc gatagacatc gggccagaac ctacataaac 60
aaagtcagac attactgagg ctgctacc atg cta gat ttt caa aac aag cgt 112
Met Leu Asp Phe Gln Asn Lys Arg
1 5
aaa tat ctg aaa agt gca gaa tcc ttc aaa gct tca ctg cgt gat aac 160
Lys Tyr Leu Lys Ser Ala Glu Ser Phe Lys Ala Ser Leu Arg Asp Asn
10 15 20
cgc act gtt att tat caa ggc caa gtt gtt gag gat gtg act aca cac 208
Arg Thr Val Ile Tyr Gln Gly Gln Val Val Glu Asp Val Thr Thr His
25 30 35 40
ttc tct acg gct gga ggc ata tcg caa gtt gca gaa atc tac gaa gaa 256
Phe Ser Thr Ala Gly Gly Ile Ser Gln Val Ala Glu Ile Tyr Glu Glu
45 50 55
caa ttc agc ggt gaa cac gac gac att ctg act tac gta cgc ccc gac 304
Gln Phe Ser Gly Glu His Asp Asp Ile Leu Thr Tyr Val Arg Pro Asp
60 65 70
ggc tac ctg gcc tct tct gcc tat atg ccc cct aga aac aaa gaa gac 352
Gly Tyr Leu Ala Ser Ser Ala Tyr Met Pro Pro Arg Asn Lys Glu Asp
75 80 85
ttg gcg tcg cga cgc cgc gca atc atg tac gtc tcg caa aaa acc tgg 400
Leu Ala Ser Arg Arg Arg Ala Ile Met Tyr Val Ser Gln Lys Thr Trp
90 95 100
ggc acc cac tgc cgt aac ctg gac atg atc gcc agc ttc acc gtc ggc 448
Gly Thr His Cys Arg Asn Leu Asp Met Ile Ala Ser Phe Thr Val Gly
105 110 115 120
atg atg gga tat ctg ccg aca ttc agg aaa aaa tgc cct gag tac gca 496

Met Met Gly Tyr Leu Pro Thr Phe Arg Lys Lys Cys Pro Glu Tyr Ala	
125 130 135	
gaa aac att acc gaa tac cat gac tac gcc gag cgc aac agc ctg tat	544
Glu Asn Ile Thr Glu Tyr His Asp Tyr Ala Glu Arg Asn Ser Leu Tyr	
140 145 150	
ttg tct gag acc att gtt gat cca cag ggc tat cgg gca cgt acc cac	592
Leu Ser Glu Thr Ile Val Asp Pro Gln Gly Tyr Arg Ala Arg Thr His	
155 160 165	
ggc acc gac ctc aac ctg ccg ccg ccc gat cgt gcc gtg atg agg atc	640
Gly Thr Asp Leu Asn Leu Pro Pro Pro Asp Arg Ala Val Met Arg Ile	
170 175 180	
aac aag cag aac gcc gag ggc atc tgg atc agc ggc gtc aaa ggc gtg	688
Asn Lys Gln Asn Ala Glu Gly Ile Trp Ile Ser Gly Val Lys Gly Val	
185 190 195 200	
ggc acg gca gca ccg cag tcc aat gaa ata ttt gtt ggc agc ttg ttc	736
Gly Thr Ala Ala Pro Gln Ser Asn Glu Ile Phe Val Gly Ser Leu Phe	
205 210 215	
ccc gca gcg ccc gag gag tca ttc tgg gct tac gtc cct gtc gat gcg	784
Pro Ala Ala Pro Glu Glu Ser Phe Trp Ala Tyr Val Pro Val Asp Ala	
220 225 230	
ccg ggg gtg aag att ttt tgc cga gag att gtc tcc cag cct cac gcc	832
Pro Gly Val Lys Ile Phe Cys Arg Glu Ile Val Ser Gln Pro His Ala	
235 240 245	
agc gcc tat gac cac ccg ctc ata tcc aaa ggt gaa gaa gcc gag gcg	880
Ser Ala Tyr Asp His Pro Leu Ile Ser Lys Gly Glu Glu Ala Glu Ala	
250 255 260	
atg gtg gta ttc gat aac gtg ttc att cca cgc tgg cga atc atg gcg	928
Met Val Val Phe Asp Asn Val Phe Ile Pro Arg Trp Arg Ile Met Ala	
265 270 275 280	
gcg aac gtg ccg gaa ctg gcc agc gcc ggc ttc ttc agt ctg tgg acc	976
Ala Asn Val Pro Glu Leu Ala Ser Ala Gly Phe Phe Ser Leu Trp Thr	
285 290 295	
tca tac agc cat tgg tac acg ctc gtg cgc ctg gaa acc aag gct gac	1024
Ser Tyr Ser His Trp Tyr Thr Leu Val Arg Leu Glu Thr Lys Ala Asp	
300 305 310	
ctg tat gcc gga ctg gcc aag gtg atc atg gaa gtc ctg ggc ctt gag	1072
Leu Tyr Ala Gly Leu Ala Lys Val Ile Met Glu Val Leu Gly Leu Glu	
315 320 325	
ggg att gcg gtg gtt cgc cag ccg gtc agc gaa ata gtg cag ctt gcg	1120
Gly Ile Ala Val Val Arg Gln Arg Val Ser Glu Ile Val Gln Leu Ala	
330 335 340	
gaa ata ctc aaa ggc atg tgc atc gcc tcc atc gaa acg gcc gag atg	1168

Glu Ile Leu Lys Gly Met Cys Ile Ala Ser Ile Glu Thr Ala Glu Met 345 350 355 360	
tcc gac ggc gac ata ttg ctg cct ggc cac aac gca ctg gcc gcc gga Ser Asp Gly Asp Ile Leu Leu Pro Gly His Asn Ala Leu Ala Ala Gly 365 370 375	1216
agg gtt ttt gcc atg gag aaa ttg cct cgg gtg ctg cat ttg ctc aga Arg Val Phe Ala Met Glu Lys Leu Pro Arg Val Leu His Leu Leu Arg 380 385 390	1264
gag ctg tgc gga cag ggc ttg atc ctc agg ttc aac gag aaa gac ttg Glu Leu Cys Gly Gln Gly Leu Ile Leu Arg Phe Asn Glu Lys Asp Leu 395 400 405	1312
gcc gcc gac gcc gcc ttt ggc cag aag ttc tcc tgg ttt ctt gac acg Ala Ala Asp Ala Ala Phe Gly Gln Lys Phe Ser Trp Phe Leu Asp Thr 410 415 420	1360
caa agc gtg ggc gcc aga gag aag aac ctg ctg atg aac cta gtg tgg Gln Ser Val Gly Ala Arg Glu Lys Asn Leu Leu Met Asn Leu Val Trp 425 430 435 440	1408
gac gtg gct gcc agt gag cac tcc aca cgt gca ttg gtg ttt gaa gaa Asp Val Ala Ala Ser Glu His Ser Thr Arg Ala Leu Val Phe Glu Glu 445 450 455	1456
cag cac gca ctc agc gag ccc ctg ctg cgc gat aac ctg gtg ctg gac Gln His Ala Leu Ser Glu Pro Leu Leu Arg Asp Asn Leu Val Leu Asp 460 465 470	1504
tac gac tac cgc gaa agc aca agc ctg ata cgc cgc cta gtg ggg ctc Tyr Asp Tyr Arg Glu Ser Thr Ser Leu Ile Arg Arg Leu Val Gly Leu 475 480 485	1552
aac gcc aaa tag acctgattgc cgtgtaggcg ccgcgcgaacc cttcattcgt Asn Ala Lys 490	1604
gccgactgaa ctccggcacga atgaagggtt gtccgcctcc ggccccaggc atcccgtaa	1664
cttccaacct tcaacggttag tacaccgccc cattagcatc caaatgaata cggcaggagc	1724
ccgttacagc gctggcgctg gatgcctggc tacgcttgca caggatctcg gtccgagacg	1784
agccagggttt accggccccc ctttgttcga gccatgccac ttggcaggct cgttcagttg	1844
tagcggtcag cctgtcgccg gttggcttgc caccgtacc gaacgtcagt agggcgcttg	1904
gtccgggttg catccgggaa tgcagtgaaa cgcgtcgcct ggttcaggc ccaggcgcca	1964
gccaacggag aaaacaaggc gctcaccagc gcccatgcac acaggcgcg cgcgctttca	2024
ataccaaagc ccaagccccg tcacagcccc ccaagcgcca cctccaggcc agcgtccagc	2084
atcggccctc gcccagaagc gccagccata tcggcacctg agcgaccagc gaaagggtca	2144

gcatggggccc gctcactggt gtacattcct cccacaggac gacacatcat ttaccagtg 2204
 aacggagttc aacgcgtggt ctgaccctc aatccgcgtc accgccggct tgccagtttc 2264
 tcgttgctag ccgtggcctt aagcctcgcc gcctgcaacg cttccgcccc ttcccataacc 2324
 gccctgcccc ccgccccgga aatcgcttgg gggtatcgca ccgacctgca agtgcagcac 2384
 gccgaccggc atatggcggc cgcggccaac ccgttggcgg ccgaagccgg gcgcgaaatg 2444
 ttgcgcaagg gtggttcggc catcgatgcg gcgattgcca tgcaagcggg gctgaccctg 2504
 gtggagccgc agtcgtcggg gatcggcggc ggcgcttga tcgtgctctg ggacggcaag 2564
 gcggtgcgca cgtacgacgg tcgcgaaacc gcgccggccg gggccaccga aaagttgttc 2624
 ctgcaagccg acggcaagcc catgccgttc cccagggcac agatcggcgg ccgttcgggtg 2684
 ggtacgcccg gcgtgctgcg cgcctggaa ctggcccatg aaaaacacgg ccgcctgccg 2744
 tgggcgcagc tggtcgagcc ggcgattcgc ctggcggacc agggtttccc gatctccccg 2804
 cgctgcaca gcatgataaa aaccgatccg tacctggcga aatcgccgga tatggccgcc 2864
 tactt 2869

<210> 2

<211> 491

<212> PRT

<213> Pseudomonas chlororaphis

<400> 2

Met Leu Asp Phe Gln Asn Lys Arg Lys Tyr Leu Lys Ser Ala Glu Ser
 1 5 10 15

Phe Lys Ala Ser Leu Arg Asp Asn Arg Thr Val Ile Tyr Gln Gly Gln
 20 25 30

Val Val Glu Asp Val Thr Thr His Phe Ser Thr Ala Gly Gly Ile Ser
 35 40 45

Gln Val Ala Glu Ile Tyr Glu Glu Gln Phe Ser Gly Glu His Asp Asp
 50 55 60

Ile Leu Thr Tyr Val Arg Pro Asp Gly Tyr Leu Ala Ser Ser Ala Tyr

65

70

75

80

Met Pro Pro Arg Asn Lys Glu Asp Leu Ala Ser Arg Arg Arg Ala Ile
 85 90 95

Met Tyr Val Ser Gln Lys Thr Trp Gly Thr His Cys Arg Asn Leu Asp
 100 105 110

Met Ile Ala Ser Phe Thr Val Gly Met Met Gly Tyr Leu Pro Thr Phe
 115 120 125

Arg Lys Lys Cys Pro Glu Tyr Ala Glu Asn Ile Thr Glu Tyr His Asp
 130 135 140

Tyr Ala Glu Arg Asn Ser Leu Tyr Leu Ser Glu Thr Ile Val Asp Pro
 145 150 155 160

Gln Gly Tyr Arg Ala Arg Thr His Gly Thr Asp Leu Asn Leu Pro Pro
 165 170 175

Pro Asp Arg Ala Val Met Arg Ile Asn Lys Gln Asn Ala Glu Gly Ile
 180 185 190

Trp Ile Ser Gly Val Lys Gly Val Gly Thr Ala Ala Pro Gln Ser Asn
 195 200 205

Glu Ile Phe Val Gly Ser Leu Phe Pro Ala Ala Pro Glu Glu Ser Phe
 210 215 220

Trp Ala Tyr Val Pro Val Asp Ala Pro Gly Val Lys Ile Phe Cys Arg
 225 230 235 240

Glu Ile Val Ser Gln Pro His Ala Ser Ala Tyr Asp His Pro Leu Ile
 245 250 255

Ser Lys Gly Glu Glu Ala Glu Ala Met Val Val Phe Asp Asn Val Phe
 260 265 270

Ile Pro Arg Trp Arg Ile Met Ala Ala Asn Val Pro Glu Leu Ala Ser
 275 280 285

Ala Gly Phe Phe Ser Leu Trp Thr Ser Tyr Ser His Trp Tyr Thr Leu

290	295	300
Val Arg Leu Glu Thr Lys Ala Asp Leu Tyr Ala Gly Leu Ala Lys Val 305 310 315 320		
Ile Met Glu Val Leu Gly Leu Glu Gly Ile Ala Val Val Arg Gln Arg 325 330 335		
Val Ser Glu Ile Val Gln Leu Ala Glu Ile Leu Lys Gly Met Cys Ile 340 345 350		
Ala Ser Ile Glu Thr Ala Glu Met Ser Asp Gly Asp Ile Leu Leu Pro 355 360 365		
Gly His Asn Ala Leu Ala Ala Gly Arg Val Phe Ala Met Glu Lys Leu 370 375 380		
Pro Arg Val Leu His Leu Leu Arg Glu Leu Cys Gly Gln Gly Leu Ile 385 390 395 400		
Leu Arg Phe Asn Glu Lys Asp Leu Ala Ala Asp Ala Ala Phe Gly Gln 405 410 415		
Lys Phe Ser Trp Phe Leu Asp Thr Gln Ser Val Gly Ala Arg Glu Lys 420 425 430		
Asn Leu Leu Met Asn Leu Val Trp Asp Val Ala Ala Ser Glu His Ser 435 440 445		
Thr Arg Ala Leu Val Phe Glu Glu Gln His Ala Leu Ser Glu Pro Leu 450 455 460		
Leu Arg Asp Asn Leu Val Leu Asp Tyr Asp Tyr Arg Glu Ser Thr Ser 465 470 475 480		
Leu Ile Arg Arg Leu Val Gly Leu Asn Ala Lys 485 490		

<210> 3

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> primer PCA2a

<400> 3

ttgccaagcc tcgctccaac

20

<210> 4

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> primer PCA3b

<400> 4

ccgcgttggt cctcgttcat

20

<210> 5

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> primer 30-84XBA

<400> 5

aagtccagat gcgaaagaac g

21

<210> 6

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> primer PHZO10

<400> 6

aagtggcatg gctcgaataa a

21

<210> 7

<211> 17

<212> DNA

<213> artificial sequence

<220>

<223> primer PHZ1

<400> 7

ggcgacatgg tcaacgg

17

<210> 8

<211> 17

<212> DNA

<213> artificial sequence

<220>

<223> primer PHZ2

<400> 8

cggctggcgg cgtattc

17

<210> 9

<211> 26

<212> DNA

<213> artificial sequence

<220>

<223> primer PHZX

<400> 9

ttttttcata tgcctgcttc gctttc

26

<210> 10

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> primer PHZY

<400> 10

tttggatcct taagttggaa tgcctccg

28

<210> 11

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> primer PHZO

<400> 11

cgactctaga acgttgtcct tgacc

25